

CLAIMS

1 1. A process for altering the host range of.
2 Bacillus toxins which comprises recombining in vitro
3 the variable region of two or more Bacillus toxin genes.

1 2. A process, according to claim 1, wherein the
2 Bacillus is a *Bacillus thuringiensis*.

1 3. A process, according to claim 2, wherein
2 variable regions of Bacillus thuringiensis var.
3 kurstaki HD-1 and Bacillus thuringiensis var.
4 kurstaki HD-73 are recombined in vitro to give genes
5 encoding chimeric toxins having altered host ranges.

1 4. DNA, denoted pEW3, encoding a chimeric toxin
2 having pesticidal activity, as follows:

| | | start | HD-73) | | ATG | GATAACAATC | 400 |
|----|------------|------------|-------------|------------|------------|------------|-----|
| 3 | CGAACATCAA | TGAATGCATT | CCTTATAATT | GTTTAAGTAA | CCCTGAAGTA | | |
| 4 | GAAGTATTAG | GTGGAGAAAG | AATAGAAACT | GGTTACACCC | CAATCGATAT | 500 | |
| 5 | TTCCTTGTG | CTAACGCAAT | TTCTTTGAG | TGAATTGTT | CCCGGTGCTG | | |
| 6 | GATTGTGTT | AGGACTAGTT | GATATAATAT | GGGGAATT | TGGTCCCTCT | 600 | |
| 7 | CAATGGGACG | CATTCTTGT | ACAAATTGAA | CAGTTAATT | ACCAAAGAAT | | |
| 8 | AGAAGAATT | GCTAGGAACC | AAGCCATTTC | TAGATTAGAA | GGACTAAGCA | 700 | |
| 9 | ATCTTATCA | AATTACGCA | GAATCTTTA | GAGAGTGGGA | AGCAGATCCT | | |
| 10 | ACTAATCCAG | CATTAAGAGA | AGAGATGCGT | ATTCAATTCA | ATGACATGAA | 800 | |
| 11 | CAGTGCCCTT | ACAACCGCTA | TTCCCTTTT | TGCAGTTCAA | AATTATCAAG | | |
| 12 | TTCCCTTTT | ATCAGTATAT | GTTCAGCTG | CAAATTACA | TTTATCAGTT | 900 | |
| 13 | TTGAGAGATG | TTTCAGTGT | TGGACAAAGG | TGGGGATTG | ATGCCGCGAC | | |
| 14 | TATCAATAGT | CGTTATAATG | ATTTAACTAG | GCTTATTGGC | AACTATACAG | 1000 | |
| 15 | ATTATGCTGT | ACGCTGGTAC | AATACGGGAT | TAGAACGTGT | ATGGGGACCG | | |
| 16 | GATTCTAGAG | ATTGGGTAAG | GTATAATCAA | TTTAAAGAG | AATTAACACT | 1100 | |
| 17 | AACTGTATTA | GATATCGTTG | CTCTGTTCCC | GAATTATGAT | AGTAGAAGAT | | |
| 18 | ATCCAATTG | AACAGTTCC | CAATTAAACAA | GAGAAATT | TACAAACCCA | 1200 | |
| 19 | GTATTAGAAA | ATTTGTATGG | TAGTTTCA | GGCTCGGCTC | AGGGCATAGA | | |
| 20 | AAGAAGTATT | AGGAGTCCAC | ATTGTATGGA | TATACTTAAC | AGTATAACCA | 1300 | |
| | TCTATACGGA | TGCTCATAGG | GGTTATTATT | ATTGGTCAGG | GCATCAAATA | | |
| | ATGGCTTCTC | CTGTAGGGTT | TTGGGGGCCA | GAATTCACTT | TTCCGCTATA | 1400 | |
| | TGGAACATG | GGAAATGCAG | CTCCACAAACA | ACGTATTGTT | GCTCAACTAG | | |
| | GTCAGGGCGT | GTATAGAAC | TTATCGTCCA | CTTTATATAG | AAGACCTTT | 1500 | |
| | AATATAGGGA | TAATAATCA | ACAACATATCT | GTTCTGACG | GGACAGAATT | | |
| | TGCTTATGGA | ACCTCCTCAA | ATTGCCATC | CGCTGTATAC | AGAAAAAGCG | 1600 | |
| | GAACGGTAGA | TTCGCTGGAT | GAAATACCGC | CACAGAATAA | CAACGTGCCA | | |

21 CCTAGGCAAG GATTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTT 1700
 22 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 (start HD-1) CCACGT TTTCTTGGCA GCATCGCAGT 1900
 23 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 24 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 25 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
 26 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 27 AATTGCTAC GCTTCTACTA CAAATTACA ATTCACATACA TCAATTGACG
 28 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 29 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA
 30 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 31 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 32 ACCTTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
 33 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 34 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
 35 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 36 ACTTAGTGTAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 37 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 38 GGAGGCATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 39 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 40 TAAAAGCCTA TACCGTTAT CAATTAAGAG GGTATATCGA AGATAATCAA 2800
 41 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 42 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900
 43 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 44 GACTTAGATT GTTGTGTAG GGATGGAGAA AAGTGTGCC ATCATTCGCA 3000
 45 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 46 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 47 CTAGGGAAATC TAGAGTTCCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 48 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200
 49 TGGAAATGGGA AACAAATATC GTTATATAAG AGGCAAAAGA ATCTGTAGAT
 50 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 51 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 52 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 53 GAATTAGAAG GGCATTTT CACTGCATTC TCCCTATATG ATGCAGAGAAA
 54 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 55 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
 56 CTCCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 57 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGGAGGGA TATGGAGAAG
 58 GTTGCCTAAC CATTGATGAG ATCGAGAACCA ATACAGACGA ACTGAAGTTT 3700
 59 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 60 TGATTATACT GTAAATCAAG AAGAATAACGG AGGTGCGTAC ACTTCTCGTA 3800
 61 ATCGAGGATA TAACGAAAGCT CCTTCCGTAC CAGCTGATTG TGCGTCAGTC
 62 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAC CTTGTGAATT 3900
 63 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 64 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 65 GAAACGGAAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 66 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54

55 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
56 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
57 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
58 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
59 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
60 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
61 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
62 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
63 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
64 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
65 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
66 P E F T F P L Y G T M G N A A P O Q R I V A Q L G Q G V Y R
67 T L S S T L Y R R F F N I G I N N Q Q L S V L D G T E F A Y
68 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
69 P P R O G F S H R L S H V S M F R S G F S N S S V S I I R A
70 P T F S W O H R S A E F N N I I P S S Q I T Q I P L T K S T
71 N L G S B T S V V K G P G F T G G D I L R R T S P G Q I S T
72 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
73 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
74 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
75 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
76 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
77 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
78 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
79 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
80 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
81 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
A A D K R V H S I R E A Y L P E L S V I F G V N A A I F E E
L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
E N N T D E L K F S N C V E E E I Y F N N T V T C N D Y T V
N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
E E K S Y T D G R R R E N P C E F N R G Y R D Y T P L P V G Y
V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
E L L L M E E.

1 5. DNA, denoted pEW4, encoding a chimeric toxin,
2 having pesticidal activity, as follows:

3 (start HD-1) ATGG ATAACAATCC GAACATCAAT
4 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
5 TGGAGAAAGA ATAGAAAAGT GTTACACCCC AATCGATATT TCCTTGTGCG
6 TAACGCAATT TCTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
7 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
8 ATTTCTGTG CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800
9 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
10 ATTTACGCGAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
11 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
12 CAACCGCTAT TCCTCTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTA 1000
13 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTT TGAGAGATGT
14 TTCAGTGTGTT GGACAAAGGT GGGGATTGTA TGCCGCGACT ATCAATAGTC 1100
15 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
16 CGCTGGTACA ATACGGGATT AGAGCGTGTG TGGGGACCGG ATTCTAGAGA 1200
17 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
18 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTGCA 1300
19 ACAGTTTCCC AATTAACAAG AGAAATTAT ACGAACCCAG TATTAGAAAA
20 TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
21 GGCACACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
22 GTGCATAGAG GCTTTAATTG TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
23 TGAGGGTTT TCAGGACCAAG AATTGCGATT CCCTTTATTT GGGAAATGCGG
24 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
25 AGAACATTAT CTTCACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCC
26 AAATAATCAG GAACTGTTG TCCTTGATGG AACGGAGTTT TCTTTGCCT 1700
27 CCCTAACGAC CAACTGCGCT TCCACTATAT ATAGACAAAG GGGTACAGTC
28 GATTCACTAG ATGTAAATACC GCCACAGGGAT AATAGTGTAC CACCTCGTGC 1800
29 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
30 GAGCAGTTA CACCTTGAGA GCTCAACGT (stop HD-1)
31 (start HD-73) CCT ATGTTCTCTT
32 GGATACATCG TAGTGTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
33 ACTCAAATCC CTGCACTGAA GGGAAACCTT CTTTTAATG GTTCTGTAAT
34 TTCAGGACCA GGATTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
35 GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
36 TCGACATCTA CCAGATATCG AGTTGCGTGT CGGTATGCTT CTGTAACCCC 2000
37 GATTCACTC AACGTTAATT GGGGTAAATTG ATCCATTGTTT TCCAATACAG
38 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100
39 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
40 TGTTAGAAAT TTTAGTGGGA CTGCAGGGAGT GATAATAGAC AGATTTGAAT 2200
41 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
42 CAGAAGGCAGG TGAATGCGCT GTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300
43 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
44 ATTATCGGA TGAATTGTTG CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
45 GTCAAACATG CGAACGCACT CAGTGATGAA CGCAATTAC TCCAAGATTC
46 AAATTTCAAA GACATTAATA GGCAACCCAGA ACGTGGGTGG GGCAGGAAGTA 2500
47 CAGGGATTAC CATCCAAGGA GGGGATGAGC TATTAAAGA AAATTACGTC
48 ACACATATCAG GTACCTTGA TGAGTGTAT CCAACATATT TGTATCAAAA 2600
49 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT
50 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTG CTACAATGCA 2700
51 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTAT GGCCGCTTTC

36 AGCCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGCGCCAC 2800
37 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
38 TGTGCCCATC ATTTCGATCA TTTCTCCCTA GACATTGATG TAGGATGTAC 2900
39 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTAAAG ATTAAGACGC
40 AAGATGGGCA CGCAAGACTA GGGAAATCTAG AGTTTCTCGA AGAGAAAACCA 3000
41 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
42 AGACAAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAAGAGG 3100
43 CAAAAAGAATC TGAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATT
44 CAAGCGGATA CGAATATTGC CATGATTTCAT CGGGCAGATA AACGTGTTCA 3200
45 TAGCATTCGA GAAGCTTATC TGCTCTGAGCT GTCTGTGATT CGGGGTGTCA
46 ATGCAGGCTAT TTTTGAAGAA TTAGAAGGGC GATTTTCAC TGCAATTCTCC 3300
47 CTATATGATG CGAGAAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
48 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
49 AACGTTCGGT CCTTGTTGTT CGGAAATGGG AAGCAGAAAGT GTCACAAGAA
50 GTTCGTGTCT GTCCGGGTGCG TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500
51 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA
52 CAGACGAACG GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600
53 AACACGGTAA CGTGTAAATGA TTATACTGTA AATCAAGAAG AATAACGGAGG
54 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700
55 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAAGA
56 GAGAATCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
57 AGTTGGTTAT GTGACAAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
58 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900
59 GAATTACTCC TTATGGAGGA A (end HD-73)

and equivalent nucleotide sequences coding for toxin
EW4 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 55 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 56 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
 57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 58 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 59 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 61 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 62 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 63 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 64 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 65 P E F A F F L F G N A G N A A F P V L V S L T G L G I F R T
 66 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
 67 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
 68 V F F R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
 69 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
 70 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
 71 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
 72 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
 73 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
 74 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
 75 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
 76 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
 77 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
 78 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
 79 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
 80 G T G S L W P E S A Q S P I G K C G E P N R C A P H L E W N
 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
 K F L V G E A L A R V K R A E K K W R D K R E K L E W E T N
 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
 S V E L L L M E E .

1 6. DNA, denoted pACB-1, encoding a chimeric toxin,
 2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400
 4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 5 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 6 TTCCCTTGTG 0 CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGTG
 7 GATTGTGTT AGGACTAGTT GATATAATAT GGGGAATT TT TGTTCCCTCT 600
 8 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
 9 AGAAGAATTG GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
 10 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
 11 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 12 CAGTGCCTT ACAACCGCTA TTCCCTTT TGCAAGTCAA AATTATCAAG
 13 TTCCCTTTT ATCAGTATAT GTTCAAGCTG CAAATTACA TTTATCAGTT 900
 14 TTGAGAGATG TTTCAGTGT TGACAAAGG TGGGGATTG ATGCCGCGAC
 15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 19 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
 20 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
 21 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 22 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 23 ATGGCCTCTC CTGTAGGGTT TTCCGGGCCA GAATTCACTT TTCCGCTATA 1400
 24 TGGAACTATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 25 GTCAGGGCGT GTATAGAACCA TTATCGTCCA CTTTATATAG AAGACCTTT 1500
 26 AATATAGGGG AATAATATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 27 TGCTTATGG A CCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 28 GAAACGGTAGA TTGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
 29 CCTAGGCAAG AATTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTT 1700
 30 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 31 (start HD-11) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 32 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT
 33 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAAG 2000
 34 GATTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
 35 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCGGGTAAG 2100
 36 AATTGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
 37 GAAGACCTAT TAATCAGGGT AATTTCAG CAACTATGAG TAGTGGGAGT 2200
 38 AATTACAGT CCGGAAGCTT TAGGACTGTG GTTTTACTA CTCCGTTAA
 39 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGTCTAT GTCTTCATT 2300
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAGTA
 41 ACCTTGTAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 42 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 43 ATCATATTGA TCAAGTATCC AATTAGTTG AGTGTTTATC AGATGAATT 2500
 44 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 45 ACTTAGTGT GAGCGGAATT TACTTCAGA TCCAAACTTC AGAGGGATCA 2600
 46 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCAA
 47 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 48 TGATGAGTGC TATCCAAACGT ATTATATATCA AAAAATAGAT GAGTCGAAAT
 49 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 50 GACTTAGAAA TCTATTTAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA
 51 TGTGCCAGGT ACGGGTTCC TATGGCCGCT TTCAAGCCAA AGTCCAATCG 2900
 52 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 53 GACTTAGATT GTTCTGTGAG GGATGGAGAA AAGTGTGCCA ATCATTGCGA 3000
 54 TCATTCTCC TTAGACATTG ATGTAGGGATG TACAGACTTA AATGAGGACC

55 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAAGGAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200
 58 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 62 GAATTAGAAG GGCCTATTTC CACTGCATTC TCCCTATATG ATGCAGAGAAA
 63 TGTCTTAAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
 65 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTGCGT TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGG TATGGAGAAG
 67 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 68 ABCAACTGCG TAGAAGAGGA AATCTATCCCA AATAAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATAACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTTCCC AAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAG GAACATTAT CGTGGACACG 6TGGAAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
 77 ACB-1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 87 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 88 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 91 G T T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
 92 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 93 P T F S W Q H R S A E F N N I P S S Q I T Q I P L T K S T
 94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G

97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I
98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
100 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
101 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
104 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
105 L D C S C R D G E K C A H H H S H H F S L D I D V G C T D L N
106 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
110 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
111 N V K G H V D V E E Q N N N Q R S V L V L P E W E A E V S Q E
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
117 E L L L M E E.

1 7. DNA, denoted pSYW1, encoding a chimeric toxin,
2 having pesticidal activity, as follows:

| | | start | HD-73) | ATG | GATAACAATC | 400 |
|----|--|-------------|-------------|-------------|------------------------|-------------------|
| 3 | | CGAACATCAA | TGAATGCATT | CCTTATAATT | GT TTAAGTAA | CCCTGAAGTA |
| 4 | | GAAGTATTAG | GTGGAGAAAG | AATAGAAACT | GGTTACACCC | CAATCGATAT |
| 5 | | TTCCTTGTG | CTAACGCAAT | TTCTTTGAG | TGAATTGTT | CCCGGTGCTG |
| 6 | | GATTTGTGTT | AGGACTAGTT | GATATAATAT | GGGGAATT | TGGTCCCTCT |
| 7 | | CAATGGGACG | CATTTCTTGT | ACAAATTGAA | CAGTTAATTA | ACCAAAGAAT |
| 8 | | AGAAGAATT | GCTAGGAACC | AAGCCATTTC | TAGATTAGAA | GGACTAAGCA |
| 9 | | ATCTTATCA | AATTTACGCA | GAATCTTTA | GAGAGTGGGA | AGCAGATCCT |
| 10 | | ACTAATCCAG | CATTAAGAGA | AGAGATGCGT | ATTCAATTCA | ATGACATGAA |
| 11 | | CAGTGCCCTT | ACAACCGCTA | TTCCCTCTTT | TGCA | GTTCAA AATTATCAAG |
| 12 | | TTCCCTCTTT | ATCAGTATA | GTTCAAGCTG | CAAATTACA | TTTATCAGTT |
| 13 | | TTGAGAGATG | TTTCAGTGT | TGGACAAAGG | TGGGGATTG | ATGCCGCGAC |
| 14 | | TATCAATAGT | CGTTATAATG | ATTTAACTAG | GCTTATTGGC | AACTATACAG |
| 15 | | ATTATGCTGT | ACGCTGGTAC | AATACGGGAT | TAGAACGTGT | ATGGGGACCG |
| 16 | | GATTCTAGAG | ATTGGGTAAG | GTATAATCAA | JTTAGAAAGAG | AA |
| 17 | | AACTGTATTA | GATATCGTTG | CTCTGTTCCC | TTAAC | AACT |
| 18 | | ATCCAATTG | ACAGTTCC | CAATTAAACAA | GAATTATGAT | AGTAGAAAGAT |
| 19 | | GTATTAGAAA | ATTTTGATGG | TAGTTTTCGA | GAGAAATT | TTAACAAACCA |
| 20 | | AGGAAGTATT | AGGAGTCCAC | ATTTGATGGA | TACAA | ACCA |
| 21 | | TCTATACGGA | TGCTCATAAA | GGGGAAATATT | GGG | CTGAGGCA |
| 22 | | ATGGSCTTCTC | CTGTAGGGTT | TTCCGGGGCCA | CACTT | TTCCGCTATA |
| 23 | | TGGAACATATG | GGAAATGCAG | CTCCACAAACA | AGCTATTGTT | GCTCAACTAG |
| 24 | | GTCAGGGCGT | GTATAGAACAA | TTATCGTCCA | CTTTATATAG | AAGACCTTTT |
| 25 | | AATATAAGGGA | TAATAATCA | ACAACATATCT | GGTCTTGACG | GGACAGAATT |
| 26 | | | | | | |

27 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAAC AGAAAAAAGCG 1600
 28 GAAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 29 CCTAGGCAAG GATTAGTC ACGATTAAGC CATGTTTCAA TGTTTGTTC 1700
 30 AGGCTTTAGT AATAGTAGTG TAAAGTATAAT AAGAGCT (end hd-73)
 31 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCACT 1900
 32 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 33 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGTTT AAAGGACCAAG 2000
 34 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
 35 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 36 AATTGCTAC GCTTCTACTA CAAATTACA ATTCGATACA TCAATTGACG
 37 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA
 39 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAGTA
 41 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 42 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAAACAGAT GTGACGGATT
 43 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 44 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 45 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 46 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 47 GGAGGCAGATG ACCTTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 48 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 49 TAAAAGCCTA TACCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 50 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 51 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAAGCCAA AGTCCAATCG 2900
 52 GAAAGTGTGG AGAGCCGAAT CGATGCGCAG CACACCTTGA ATGGAATCCT
 53 GACTTAGATT GTTGTGTAG GGATGGAGAA AAGTGTGCCCG ATCATTGCGA 3000
 54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 55 TAGGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200
 58 TGGAAATGGGA AACAAATATC GTTGTAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTTC TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCATGATT CATGCGGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 62 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 63 TGTCAATTAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCCCTGTT
 65 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAAGTTCGTG TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGGAGGGAA TATGGAGAAAG
 67 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTG TGCGTCAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAACATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
77 SYW1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
80 V D I I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
87 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
88 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
89 P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
91 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
92 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
93 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
100 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
101 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
104 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
106 E D L G Y W V I F K I K T Q D G H A R L G N L E F L E E K P
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
110 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
117 E L L L M E E .

1 8. A chimeric toxin, EW3, having pesticidal
2 activity, having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 F V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
17 P P R O G F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A P L G N L E F L E E K P
32 L V G E S P L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A F E S V P A L F V N S Q Y D O L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E D N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 and muteins thercof which do not alter the protein
44 secondary structure.

1 9. A chimeric toxin, EW4, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNINECIPYNCLSNPPEVEVLGGERIE
4 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL
5 VDIIWGIIFGPSQWDAFPVQIEQLINQRRIEE
6 FARNQAIISRLEGLSNLYQIYAESFREWEAD
7 PTNPFALREEMRIQFNDMNSALTATIPLLA
8 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
9 RWGFDAAATINSRYNDLTRLIGNYTDYAVRW
10 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
11 LDIVALFSNYDSRRYPIRTVSQLTREIYTN
12 PVLENFDGSFRGMAQRIEONIRQPHLMDIL
13 NSITIYTDVHRGFNYWSGHQITASPVGFSG
14 PEFAFFLFGNAGNAAPPVVLVSLTGLGIFRT
15 LSSPLYRRILGSGPNNQELFVLDGTEFSF
16 ASLTTLPLSTIYRQRGTVDSLVDVIPPQDNS
17 VPPFRAGFSHRLSHVTMLSQAAGAVYTLRAQ
18 RPMFSWIHRSAEFNNIIASDSITQIPIAVKG
18 NFLFNGSVVISGPGFTGGDVLVRLNSSGNNIQ
20 NRGYIEVPIHFPSNSTSTRYRVRVRYASVTP
21 HLNVNWGNSSIFSNTVPATATSLDNLQSSD
22 FGYFESANAFTSSLGNIVGVRNFSGTAGVI
23 IDRFEFIPVTATLEAEYNLERAQKAVNALF
24 TSTNQLGLKTNVTDYHIDQVSNLVTLYSDE
25 FCLDEKRELSEKVKHAKRLSDERNLLQDSN
26 FKDINRQPGERGGGSTGITIQQGDDVFKEN
27 YVTLSGTFDECYPTYLYQKIDESKLKAFTR
28 YQLRGYIEEDSQDLEIYLIYNAKHETVNVP
29 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWN
30 PDLDCCSCRDGEGKCAHHSHHFSLDDIDVGCTD
31 LNEDLGVWVIFKIKTQDGHARLGNLEFLEE
32 KPLVGEALARVKRAEKKWRDKREKLEWETN
33 IVYKEAKESVDAFLVNSQYDQLQADTNIAM
34 IHAADKRVHSIREAYLPELSVIPGVNAAIF
35 EELERGRIFTAFSLYDARNVIKNGDFNNGLS
36 CWNVKGHVDVEEQQNQRSQLVVPEWEAEVS
37 QEVRVCPGRGYILRVTAYKEGYGEGCVTIH
38 EIENNNTDELKFSNCVEEEIYPNNNTVTCNDY
39 TVNQEELYGGAYTSRNRGYNEAPSVPADYAS
40 VYEEKSYTGDGRRENPCCEFNRGYRDYTPLPV
41 GYVTKELEYFFETDKVWIEIGETEGTFIVD
42 SVELLLMEE

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 10. A chimeric toxin, ACB-1, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNI N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
17 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29 G S L W F L S A Q S P I G K C G E F N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 11. A chimeric toxin, SYW1, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNI N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
13 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 12: A pesticidal composition comprising pesti-
2 cide-containing substantially intact cells having
3 prolonged pesticidal activity when applied to the
4 environment of a target pest, wherein said pesticide,
5 is a chimeric toxin, is intracellular and is produced
6 as a result of expression of a heterologous gene
7 encoding said chimeric toxin in said cell.

1 13. A pesticidal composition according to claim 12,
2 wherein said cells are killed under protease deacti-
3 vating or cell wall strengthening conditions, while
4 retaining pesticidal activity.

1 14. A pesticidal composition, according to claim 12,
2 wherein said cells are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 15. A pesticidal composition, according to claim 14,
2 wherein said prokaryote is a Bacillus specie selected
3 from a pesticide-producing strain of Bacillus thurin-
4 giensis, consisting of B. thuringiensis M-7, B. thurin-
5 giensis var. kurstaki, B. thuringiensis var. finitimus,
6 B. thuringiensis var. alesti, B. thuringiensis var.
7 sotto, B. thuringiensis var. dendrolimus, B. thurin-
8 giensis var. kenyae, B. thuringiensis var. galleriae,
9 B. thuringiensis var. canadensis, B. thuringiensis var.
10 entomocidus, B. thuringiensis var. subtoxicus, B.
11 thuringiensis var. aizawai, B. thuringiensis var. morri-
12 soni, B. thuringiensis var. ostriniae, B. thuringiensis
13 var. tolworthi, B. thuringiensis var. darmstadiensis,

14 B. thuringiensis var. toumanoffi, B. thuringiensis var.
15 kyushuensis, B. thuringiensis var. thompsoni, B.
16 thuringiensis var. pakistani, B. thuringiensis var.
17 israelensis, B. thuringiensis var. indiana, B. thurin-
18 giensis var. dakota, B. thuringiensis var. tohokuensis,
19 B. thuringiensis var. kumanotoensis, B. thuringiensis
20 var. tochigiensis, B. thuringiensis var. colmeri,
21 B. thuringiensis var. wuhanensis, B. thuringiensis
22 var. tenebrionis, B. thuringiensis var. thuringiensis,
23 and other Bacillus species selected from B. cereus, B.
24 moritai, B. popilliae, B. lentimorbus, and B. sphaericus.

1 16. A method of protecting plants against pests
2 which comprises applying to said plants an effective
3 amount of a pesticidal composition comprising pesti-
4 cide-containing substantially intact unicellular
5 microorganisms, wherein said pesticide is a chimeric
6 toxin, is intracellular, and is produced as a result
7 of expression of a heterologous gene encoding said
8 chimeric toxin in said microorganism, and said micro-
9 organism is treated under conditions which prolong
10 the pesticidal activity when said composition is applied
11 to the environment of a target pest.

1 17. A method according to claim 16, wherein said
2 microorganisms are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes, selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 18. A method according to claim 16, wherein said
2 unicellular microorganisms are killed under protease
3 deactivating or cell wall strengthening conditions,
4 while retaining pesticidal activity.

1 19. Substantially intact unicellular microorganism
2 cells containing an intracellular chimeric toxin, which
3 toxin is a result of expression of a heterologous
4 gene encoding said chimeric toxin, wherein said cells
5 are killed under protease deactivating or cell wall
6 strengthening conditions, while retaining pesticidal
7 activity when said cell is applied to the environment
8 of a target pest.

1 20. Cells according to claim 19, wherein said
2 microorganism is a Pseudomonad and said toxin is
3 derived from a *B. thuringiensis*.

1 21: A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW3, encoding a
3 chimeric toxin, is as follows:

| | | (start | HD-73) | ATG | GATAACAATC | 400 |
|----|------------|------------|------------|-------|------------|------------|
| 4 | CGAACATCAA | TGAATGCATT | CCTTATAATT | GT | TTAAGTAA | CCCTGAAGTA |
| 5 | GAAGTATTAG | GTGGAGAAAG | AATAGAAA | GG | TTACACCC | CAATCGATAT |
| 6 | TTCCTTGTG | CTAACGCAAT | TTCTTTGAG | TGA | ATTGTT | CCCGGTGCTG |
| 7 | GATTTGTGTT | AGGACTAGTT | GATATAATAT | GGGG | AAATTTT | TGGTCCCTCT |
| 8 | CAATGGGACG | CATTTCTTGT | ACAAATTGAA | CAG | TAAATT | ACCAAAGAAT |
| 9 | AGAAGAATT | GCTAGGAACC | AAGCCATT | TAG | ATTAGAA | GGACTAAGCA |
| 10 | ATCTTATCA | AATTTACGCA | GAATCTTTA | GAG | AGTGGGA | AGCAGATCCT |
| 11 | ACTAATCCAG | CATTAAGAGA | AGAGATGCGT | AT | TCAATTCA | ATGACATGAA |
| 12 | CAGTGCCTT | ACAACCGCTA | TTCTCTTT | TG | CAGTTCAA | AATTATCAAG |
| 13 | TTCTCTTT | ATCAGTATAT | GTTCAGCTG | CAA | ATTTACA | TTTATCAGT |
| 14 | TTGAGAGATG | TTTCAGTGTT | TGGACAAAGG | TGGG | GGATTG | ATGCCGCGAC |
| 15 | TATCAATAGT | CGTTATAATG | ATTTAACTAG | GCTT | TATTGGC | AACTATACAG |
| | ATTATGCTGT | ACGCTGGTAC | AATACGGGAT | TAGA | ACGTGT | ATGGGGACCG |
| | GATTCTAGAG | ATTGGGTAAG | GTATAATCAA | TTT | AGAAGAG | AATTAACACT |
| | AACTGTATTA | GATATCGTTG | CTCTGTTCCC | GAATT | TATGAT | AGTAGAAGAT |
| | ATCCAATTG | AACAGTTCC | CAATTAACAA | GAGAA | ATT | TACAAACCCA |
| | GTATTAGAAA | ATTTTGATGG | TAGTTTTCGA | GGCTC | GGCTC | AGGGCATAGA |

16 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 17 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
 18 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 19 TGGAACATATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 20 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500
 21 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 22 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 23 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 24 CCTAGGCAG GATTTAGTCA TCGATTAAAGC CATGTTCAA TGTTTCGTT 1700
 25 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 26 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 27 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT 2000
 28 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAAG 2100
 29 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
 30 ACCTTAAGAG TAAATATTAC TGCAACCATTA TCACAAAGAT ATCGGGTAAG 2200
 31 AATTGCGTAC GCTTCTACTA CAAATTACAA ATTCCATACA TCAATTGACG
 32 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2300
 33 AATTTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA
 34 CTTTTCAAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2400
 35 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAAGTA
 36 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2500
 37 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 38 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2600
 39 TGTCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG
 40 ACTTAGTGAT GAGCGGAATT TACTTCAGA TCCAAACTTC AGAGGGATCA 2700
 41 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 42 GGAGGCAGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2800
 43 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 44 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2900
 45 GACTTAGAAA TCTATTTAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA
 46 TGTGCCAGGT ACGGGTTCTT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 3000
 47 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 48 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCA ATCATTGCA 3100
 49 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTA AATGAGGACC
 50 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3200
 51 CTAGGGAAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 52 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT
 53 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 54 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 55 TGCCATGATT CATGCGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 56 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGSC TATTTTGAA 3400
 57 GAATTAGAAG GGCAGTATTT CACTGCATTC TCCCTATATG ATGCAGAGAAA
 58 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 59 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTGTT
 60 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 61 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG
 62 GTTGCCTAAC CATTCAATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 63 AGCAACTCGC TAGAAGAGGAA AATCTATCCA AATAACACGG TAACGTGTAA
 64 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 65 ATCGAGGATA TAACGAAGCT CCTTCCCGTAC CAGCTGATT TGCGTCAGTC
 66 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 67 TAACAGAGGG TATAAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 68 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 69 GAAACCGGAAG GAACATTAT CGTGGACACGC GTGGAAATTAC TCCTTATGGA
 70 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
55 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
56 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
58 P T N P A L R E E M R I Q F N D M M N S A L T T A I P L F A V
59 Q N Y Q V P F L L S V Y V Q A A N L H L S V L R D V S V F G Q
58 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
59 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
60 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
60 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
61 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
61 P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
62 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
63 G T S S N L F P S A V Y R K S G T V D S L D E I P P Q N N N V
63 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
64 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
65 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
65 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
66 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
67 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
67 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
68 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
69 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
69 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
70 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
70 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
71 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
72 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
72 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
73 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
74 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
74 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
75 L E G R I F T A F S L Y D A R N V I K N G I F N N G L S C W
76 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
77 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
77 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
78 N Q E E Y G G A Y T S R N R G Y N E A F S V P A D Y A S V Y
78 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
79 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
80 E L L L M E E.

1 22. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW4, encoding a
3 chimeric toxin, is as follows:

| | | | | |
|----|---------------|-------------|-------------|-------------|
| 4 | (start HD-1) | ATGG | ATAACAATCC | GAACATCAAT |
| 5 | GAATGCATTC | CTTATAATTG | TTTAAGTAAAC | CCTGAAGTAG |
| 6 | TGGAGAAAGA | ATAGAAAATCG | GTACACCCCC | AATCGATATT |
| 7 | TAACCGAATT | TCTTTGAGT | GAATTTGTT | CCGGTGCTGG |
| 8 | GGACTAGTTG | ATATAATATG | GGGAATTTTT | GGTCCCTCTC |
| 9 | ATTTCCGTGA | CAAATTGAAC | AGTTAATTAA | CCAAAGAATA |
| 10 | CTAGGAACCA | AGCCATTCT | AGATTAGAAG | GACTAAGCAA |
| 11 | ATTTACGCGAG | AATCTTTAG | AGAGTGGGAA | GCAGATCCTA |
| 12 | ATTAAGAGAA | GAGATGCGTA | TTCATTCAA | TGACATGAAC |
| 13 | CAACCGCTAT | TCCTCTTTG | GCAGTTCAAA | ATTATCAAGT |
| 14 | TCAGTATATG | TTCAAGCTGC | AAATTACAT | TTATCAGTTT |
| 15 | TTCAGTGTGTT | GGACAAAGGT | GGGGATTGTA | TGCCGCGACT |
| 16 | GTTATAATGA | TTTAACCTAGG | CTTATTGGCA | ACTATACAGA |
| 17 | CGCTGGTACA | ATACGGGATT | AGAGCGTGT | TGGGGACCGG |
| 18 | TTGGGTAAGG | TATAATCAAT | TTAGAAGAGA | GCTAACACTT |
| 19 | ATATCGTTGC | TCTATTCTCA | AATTATGATA | GTCGAAGGTA |
| 20 | ACAGTTCC | AATTAAACAAG | AGAAAATTAT | ACGAACCCAG |
| 21 | TTTTGATGGT | AGTTTCGTT | GAATGGCTCA | GAGAATAGAA |
| 22 | GGCAACCACA | TCTTATGGAT | ATCCTTAATA | GTATAACCAT |
| 23 | GTGCATAGAG | GCTTTAATT | TTGGTCAGGG | CATCAAATAA |
| 24 | TGTAGGGTTT | TCAGGACCAAG | AATTGCGATT | CCCTTTATT |
| 25 | GGAATGCAGC | TCCACCCGTA | CTTGTCTCAT | TAACTGGTTT |
| 26 | AGAACATTAT | CTTCACCTT | ATATAGAAGA | TTTAACTTG |
| 27 | AAATAATCAG | GAACGTGTTG | TCCTTGATGG | AACGGAGTTT |
| 28 | CCCTAACGAC | CAACTTGCT | TCCACTATAT | ATAGACAAAG |
| 29 | GATTCACTAG | ATGTAATACC | GCCACAGGAT | AATAGTGTAC |
| | GGGATTTCAGC | CATCGATTGA | GTCATGTTAC | CACCTCGTGC |
| | GAGCAGTTA | CACCTTGAGA | GCTCAACGT | (stop HD-1) |
| | (start HD-73) | | CCT | ATGTTCTCTT |
| 23 | GGATACATCG | TAGTGCTGAA | TTTAATAATA | TAATTGCATC |
| 24 | ACTCAAATCC | CTGCAGTGAA | GGGAAACCTT | CTTTTTAATG |
| 25 | TTCAGGACCA | GGATTTACTG | GTGGGGACTT | AGTTAGATTA |
| 26 | GAAATAACAT | TCAGAATAGA | GGGTATATTG | AAGTCCAAT |
| 27 | TCGACATCTA | CCAGATATCG | AGTTCTGTA | CGGTATGCTT |
| 28 | GATTCACTC | AACGTTAATT | GGGGTAATT | ATCCATT |
| 29 | TACCAAGCTAC | AGCTACGTC | TTAGATAATC | TACAATCAAG |
| | TATTTGAAA | GTGCCAATGC | TTTTACATCT | TCATTAGGTA |
| | TGTTAGAAAT | TTTAGTGGGA | CTGCAGGAGT | ATATAGTAGG |
| | TTATTCCAGT | TACTGCAACA | CTCGAGGCTG | GATAATAGAC |
| | | | AATATAATCT | AGATTGAAAT |
| | | | | GGAAAGAGCG |

30 CAGAAGGCAGG TGAATGCGCT GTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300
 31 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 32 ATTTATCGGA TGAATTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 33 GTCAAACATG CGAAGCGACT CAGTGTGAA CGCAATTAC TCCAAGATTC
 34 AAATTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500
 35 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 36 ACACTATCAG GTACCTTGA TGAGTGTCTAT CCAACATATT TGTATCAAA 2600
 37 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
 38 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTG TGACAATGCA 2700
 39 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCCGCTTC
 40 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 41 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAAG
 42 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 43 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 44 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 45 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 46 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 47 CAAAAGAATC TGAGATGCT TTATTTGAA ACTCTCAATA TGATCAATTA
 48 CAAGCGGATA CGAATATTGC CATGATTCAAT GCGGCAGATA AACGTGTTCA 3200
 49 TAGCATTCGA GAAGCTTATC TGCGCTGAGCT GTCTGTGATT CGGGGTGTCA
 50 ATGCGGCTAT TTTGAAAGAA TTAGAAGGGC GTATTTTCAC TGCAATTCTCC 3300
 51 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTA ATAATGGCTT
 52 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 53 AACGTTCGGT CCTTGTGTT CCGGAATGGG AAGCAGAAAGT GTCACAAGAA
 54 GTTCGTGTCT GTCCGGGTG TGCGCTATATC CTTCGTGTCA CAGCGTACAA 3500
 55 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA
 56 CAGACGAACG GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 57 AACACGGTAA CGTGTAAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 58 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCT TCCGTACCAAG 3700
 59 CTGATTATGC GTCACTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 60 GAGAATCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 61 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
 62 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900
 63 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 55 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 56 V D I I W G I F G P S Q W D A F F P V Q I E Q L I N Q R I E E
 57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 58 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 59 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 61 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T

62 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
63 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
64 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
65 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
66 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
67 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
68 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
69 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
70 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
71 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
72 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
73 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
74 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
75 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
76 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
77 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
78 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
79 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N M
80 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
81 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
82 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
83 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
84 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
85 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
86 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
87 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
88 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
89 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
90 S V E L L L M E E .

1 23. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pACB-1, encoding a
3 chimeric toxin, is as follows:

| | | | | | |
|----|------------|---------------|------------|------------|------------|
| | | (start HD-73) | ATG | GATAACAATC | 400 |
| 4 | CGAACATCAA | TGAATGCATT | CCTTATAATT | GTTTAAGTAA | CCCTGAAGTA |
| 5 | GAAGTATTAG | GTGGAGAAAG | AATAGAAACT | GGTTACACCC | CAATCGATAT |
| 6 | TTCCTTGTG | CTAACGCAAT | TTCTTTGAG | TGAATTGTT | CCCGGTGCTG |
| 7 | GATTTGTGTT | AGGACTAGTT | GATATAATAT | GGGGAATT | TGGTCCCTCT |
| 8 | CAATGGGACG | CATTTCTTGT | ACAAATTGAA | CAGTTAATT | ACCAAAGAAT |
| 9 | AGAAGAATT | GCTAGGAACC | AAGCCATTTC | TAGATTAGAA | GGACTAAGCA |
| 10 | ATCTTATCA | AATTTACGCA | GAATCTTTA | GAGAGTGGGA | AGCAGATCCT |
| 11 | ACTAATCCAG | CATTAAGAGA | AGAGATGCGT | ATTCAATTCA | ATGACATGAA |
| 12 | CAGTCCCTT | ACAACCGCTA | TTCCCTCTTT | TGCAGTTCAA | AATTATCAAG |
| 13 | TTCCCTTTT | ATCAGTATAT | GTTCAAGCTG | CAAATTACA | TTTATCAGTT |
| 14 | TTGAGAGATG | TTTCAGTGT | TGGACAAAGG | TGGGGATTTG | ATGCCGCGAC |
| 15 | | | | | |

16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 17 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG
 18 GATTCTAGAG ATTGGGTAAG STATAATCAA TTTAGAAGAG AATTAACACT 1100
 19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 20 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
 21 STATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
 22 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 23 TCTATAACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
 24 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 25 TGGAACTATG GGAAATGCA CGTCCACAACA ACGTATTGTT GCTCAACTAG
 26 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAAGCG 1600
 29 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
 30 CCTAGGCAAG AATTAGTCA TCGATTAAGC CATGTTCAA TGTTCGTTC 1700
 31 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 32 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 33 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT
 34 AACAAAAATCT ACTAATCTTG BCTCTGGAAC TTCTGTCGTT AAAGGACCAAG 2000
 35 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTC
 36 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCGGGTAAG 2100
 37 AATTGCTTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 38 GAAGACCTAT TAATCAGGAG AATTTCAG CAACTATGAG TAGTGGGAGT 2200
 39 AATTTACAGT CGGAAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA
 40 CTTTCAAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT STCTTCATT 2300
 41 CAGGCAATGAG AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 42 ACCTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 45 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCCAAGCG
 46 ACTTAGTGTAG GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 47 ATAGACAACG AGACCGTGCG TGGAGAGGAA GTACGGATAT TACCATCCAA
 48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTC 2800
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 52 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAAGCCCAA AGTCCAATCG 2900
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 54 GACTTAGATT GTTGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTCGCA 3000
 55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGGACC
 56 TAGGTGTATG BGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 57 CTAGGGAAATC TAGAGTTCTC CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAT 3200
 59 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 60 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 63 GAATTAGAAG GGCCTATTG CACTGCATT TCCCTATATG ATGCGAGAAA
 64 TGTCATTAAGA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT

66 CTTCCGGAAT GGGAAACAGA AGTGTACAA GAAGTTCTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGG TATGGAGAAG
 68 GTTGCCTAAC CATTCACTGAG ATCGAGAAACA ATACAGACGA ACTGAAGTTT 3700
 69 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCCTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCGCTAC CAGCTGATTAA TGCCTCAGTC
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAAGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCC AAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAG GAACATTTAT CGTGGACACGC GTGGAATTAC TCCTTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 ACB-1 with the following amino acid sequence:

79 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 83 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 88 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 89 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 92 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
 93 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 102 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 105 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
 106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 107 E D L G Y W V I F K I K T Q D G H A R L G N L E F L E E K P
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E

111 'LEGRIIFTAFLSYDARNVIKNGDFNNGLSCLW
112 NVKGHVDOVEEQNNQRSQLVLPWEAEVSQE
113 VRVCPGRGYILRVTAYKEGYGEGCVTIHEI
114 ENNTDELKFNSNCVEEEIYPNNNTVTCNDYTIV
115 NQEEYGGAYTSRNRGYNEAPSVFADYASVY
116 EEKSYTDGRRENPCFNRGYRDYTPLPVGY
117 VTKELEYFPETDOKVWIEIGETEGTFIVDSV
118 ELLLMEEE.

1 24. A pesticidal composition, according to
2 claim 12, wherein said gene, denoted pSYW1, encoding
3 a chimeric toxin, is as follows:

| | | | | | | |
|----|---------------|-------------|-------------|------------|-------------|------|
| 4 | (start HD-73) | | ATG | GATAACAATC | 400 | |
| 5 | CGAACATCAA | TGAATGCATT | CCTTATAATT | GTTTAAGTAA | CCCTGAAGTA | |
| 6 | GAAGTATTAG | GTGGAGAAAAG | AATAGAAAAC | GGTTACACCC | CAATCGATAT | 500 |
| 7 | TTCCCTTGTG | CTAACGCAAT | TTCTTTGAG | TGAATTGTT | CCCGGTGCTG | |
| 8 | GATTGTGTT | AGGACTAGTT | GATATAATAT | GGGGAATTTT | TGGTCCCTCT | 600 |
| 9 | CAATGGGACG | CATTCTTGT | ACAAATTGAA | CAGTTAATT | ACCAAAGAAT | |
| 10 | AGAAGAATT | GCTAGGAACC | AAGCCATTTC | TAGATTAGAA | GGACTAAGCA | 700 |
| 11 | ATCTTATCA | AATTACGCA | GAATCTTTA | GAGAGTGGGA | AGCAGATCCT | |
| 12 | ACTAATCCAG | CATTAAGAGA | AGAGATGCGT | ATTCAATTCA | ATGACATGAA | 800 |
| 13 | CAGTGCCTT | ACAACCGCTA | TTCCCTTTT | TGCAGTTCAA | AATTATCAAG | |
| 14 | TTCCCTTTT | ATCAGTATAT | GTCAAGCTG | CAAATTACA | TTTATCAGTT | 900 |
| 15 | TTGAGAGATG | TTTCAGTGT | TGGACAAAGG | TGGGGATTTG | ATGCCGCGAC | |
| 16 | TATCAATAGT | CGTTATAATG | ATTTAACTAG | GCTTATTGGC | AACTATACAG | 1000 |
| 17 | ATTATGCTGT | ACGCTGGTAC | AATACGGGAT | TAGAACGTGT | ATGGGGACCG | |
| 18 | GATTCTAGAG | ATTGGGTAAG | GTATAATCAA | TTAGAAAGAG | AATTAACACT | 1100 |
| 19 | AACTGTATTA | GATATCGTT | CTCTGTTCCC | GAATTATGAT | AGTAGAAAGAT | |
| 20 | ATCCAATTG | AACAGTTTCC | CAATTAAACAA | GAGAAATTAA | TACAAACCCA | 1200 |
| 21 | GTATTAGAAA | ATTTGATGG | TAGTTTTCGA | GGCTCGGCTC | AGGGCATAGA | |
| 22 | AGGAAGTATT | AGGAGTCCAC | ATTGATGGA | TATACTTAAC | AGTATAACCA | 1300 |
| 23 | TCTATACGGA | TGCTCATAAA | GGGGAAATATT | ATTGGTCAGG | GCATCAAATA | |
| 24 | ATGGCTTCTC | CTGTAGGGTT | TTCGGGGCCA | GAATTCACTT | TTCCGCTATA | 1400 |
| 25 | TGGAACTATG | GGAAATGCAG | CTCCACAACA | ACGTATTGTT | GCTCAACTAG | |
| 26 | GTCAGGGCGT | GTATAGAACAA | TTATCGTCCA | CTTTATATAG | AAGACCTTT | 1500 |
| 27 | AATATAGGGA | TAATAATCA | ACAACATATCT | GTTCTTGACG | GGACAGAATT | |
| 28 | TGCTTATGGA | ACCTCCTCAA | ATTGCCATC | CGCTGTATAC | AGAAAAAGCG | 1600 |
| 29 | GAACGGTAGA | TTCGCTGGAT | GAAATACCGC | CACAGAATAA | CAACGTGCCA | |
| 30 | CCTAGGCAG | GATTTAGTCA | TCGATTAAGC | CATGTTTCAA | TGTTTCGTT | 1700 |
| 31 | AGGCTTTAGT | AATAGTAGTG | TAAGTATAAT | AAGAGCT | (end hd-73) | |
| 32 | (start HD-1) | | CCAACGT | TTTCTTGGCA | GCATCGCACT | 1900 |
| 33 | GCTGAATTAA | ATAATATAAT | TCCTTCATCA | CAAATTACAC | AAATACCTTT | |
| 34 | AACAAAATCT | ACTAATCTG | GCTCTGGAAC | TTCTGTCGTT | AAAGGACCAAG | 2000 |
| 35 | GATTACAGG | AGGAGATATT | CTTCGAAGAA | CTTCACCTGG | CCAGATTTC | |
| 36 | ACCTTAAGAG | TAATAATTAC | TGCAACATTA | TCACAAAGAT | ATCGGGTAAG | 2100 |
| 37 | AATTGCGCTAC | GCTTCTACTA | CAAATTTACA | ATTCCATACA | TCAATTGACG | |
| 38 | GAAGACCTAT | TAATCAGGGT | ATTTTTTCAG | CAACTATGAG | TAGTGGGAGT | 2200 |
| 39 | AATTTACAGT | CCGGAAAGCTT | TAGGACTGT | GGTTTTACTA | CTCCGTTAA | |
| 40 | CTTTTCAAAT | GGATCAAGTG | TATTTACGTT | AAGTGCTCAT | GTCTTCAATT | 2300 |
| 41 | CAGGCAATGA | AGTTTATATA | GATCGAATTG | AATTGTTCC | GGCAGAAGTA | |

42 ACCTTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
45 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
47 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
48 GGAGGCAGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
51 GACTTAGAGAA TCTATTAAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
52 TGTGCCAGGT ACGGGTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
53 GAAAGTGTGG AGAGCCGAAT CGATGCGCAGC CACACCTTGA ATGGAATCCT
54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCA 3000
55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
56 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
57 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
58 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200
59 TGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
60 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCCTT
62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTGGAA 3400
63 GAATTAGAAG GGCCTATTT CACTGCATTC TCCCTATATG ATGCGAGAAA
64 TGTCATTAAG AATGGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
66 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGGAGGGG TATGGAGAAG
68 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
69 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
71 ATCGAGGATA TAACGAAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900
73 TAACAGAGGG TATAGGGATT ACACGCAACT ACCAGTTGGT TATGTGACAA
74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
75 GAAACCGGAAG GAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
78 SYW1 with the following amino acid sequence:

79 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
83 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V
84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
88 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
89 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
92 G T S S N L F S A V Y R K S G T V D S L D E I P P Q N N N V
93 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
102 S I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
105 G S L W P L S A Q S P I G K C G E F P N R C A P H L E W N P D
106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
107 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
114 E N N T D E L K F S N C V E E E I Y P N N N T V T C N D Y T V
115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L R V G Y
117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
118 E L L L M E E .

25. A recombinant DNA transfer vector comprising DNA having the following nucleotide sequence or equivalent nucleotide sequences containing bases whose translated region codes for the same amino acid sequence:

| | | (start HD-73) | ATG | GATAACAATC | 400 |
|----|------------|---------------|-------------|------------|-------------|
| 5 | CGAACATCAA | TGAATGCATT | CCTTATAATT | GTTTAAGTAA | CCCTGAAGTA |
| 6 | GAAGTATTAG | GTGGAGAAAAG | AATAGAAAACT | GGTTACACCC | CAATCGATAT |
| 7 | TTCCTTGTG | CTAACGCAAT | TTCTTTGAG | TGAATTGTT | CCCGGTGCTG |
| 8 | GATTGTGTT | AGGACTAGTT | GATATAATAT | GGGGAATT | TGGTCCCTCT |
| 9 | CAATGGGACG | CATTCTTGT | ACAAATTGAA | CAGTTAATT | ACCAAAGAAT |
| 10 | AGAAGAATT | GCTAGGAACC | AAGCCATTTC | TAGATTAGAA | GGACTAAGCA |
| 11 | ATCTTATCA | AATTACGCA | GAATCTTTA | GAGAGTGGGA | AGCAGATCCT |
| 12 | ACTAATCCAG | CATTAAGAGA | AGAGATGCGT | ATTCAATTCA | ATGACATGAA |
| 13 | CAGTGCCTT | ACAACCGCTA | TTCCCTCTTT | TGCAGTTCAA | AATTATCAAG |
| 14 | TTCCCTCTTT | ATCAGTATAT | GTCAAGCTG | CAAATTACA | TTTATCAGTT |
| 15 | TTGAGAGATG | TTTCAGTGT | TGGACAAAGG | TGGGGATTG | ATGCCGCGAC |
| 16 | TATCAATAGT | CGTTATAATG | ATTTAACTAG | GCTTATTGGC | AACTATACAG |
| 17 | ATTATGCTGT | ACGCTGGTAC | AATACGGGAT | TAGAACGTGT | ATGGGGACCG |
| 18 | GATTCTAGAG | ATTGGGTAAG | GTATAATCAA | TTAGAACGAG | AATTAAACACT |
| 19 | AACTGTATTA | GATATCGTT | CTCTGTTCCC | GAATTATGAT | AGTAGAACGAT |
| 20 | ATCCAATTG | AACAGTTCC | CAATTAACAA | GAGAAATT | TACAAACCCA |
| 21 | GTATAGAAA | ATTTGATGG | TAGTTTCGA | GGCTCGGCTC | AGGGCATAGA |

23 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 24 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 25 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 26 TGGAACTATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 27 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500
 28 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 29 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 30 GAACGGTAGA TTCGCTGGAT GAAATACCAGC CACAGAATAA CAACGTGCCA
 31 CCTAGGCAAG GATTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTC 1700
 32 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 33 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 34 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT
 35 AACAAAATCT ACTAATCTTG GCTCTGAAAC TTCTGTCGTT AAAGGACCAAG 2000
 36 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTC
 37 ACCTTAASAG TAAATATTAC TGCAACCATTA TCACAAAGAT ATCAGGTAAG 2100
 38 AATTTCGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
 39 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 40 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA
 41 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300
 42 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 43 ACCTTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
 44 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 45 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 46 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 47 ACTTAGTGTG GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 48 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 49 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 50 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 51 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 52 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 53 TGTGCCAGGT ACGGGTTCTC TATGCCCGCT TTCAGCCCAA AGTCCAATCG 2900
 54 GAAAAGTGTGG AGAGCGGAAT CGATCGCGC CACACCTGAA ATGGAATCCT
 55 GACTTAGATT GTTCGTTGAG GGATGGAGAA AAGTGTGCCC ATCATTGCA 3000
 56 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 57 TAGGTGTATG BGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 58 CTAGGGAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 59 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 60 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 61 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 62 TGCCATGATT CATGCGGCAG ATAAACGTGT TCAATAGCATT CGAGAAGCTT
 63 ATCTGCCTGA GCTGCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 64 GAATTAGAAG GGCATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 65 TGTCAATTAA AATGGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 66 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTT
 67 CTTCCGGAAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 68 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG
 69 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 70 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 71 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 72 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTAA TGCCTCAGTC
 73 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 74 TAACAGAGGG TATAGGGATT ACACGCGACT ACCAGTTGGT TATGTGACAA
 75 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 76 GAAACGGGAAG GAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
 77 GGAA (end HD-1).

1 26. A recombinant DNA transfer vector comprising
2 DNA having the following nucleotide sequence or
3 equivalent nucleotide sequences containing bases whose
4 translated region codes for the same amino acid sequence:

5 (start HD-1) ATGG ATAACAATCC GAACATCAAT
6 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
7 TGGAGAAAAA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTGCGC
8 TAACGCAATT TCTTTGAGT GAATTGTTTC CCGGTGCTGG ATTTGTGTTA 700
9 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
10 ATTTCCTGTA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800
11 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
12 ATTTACGCGAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
13 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
14 CAACCGCTAT TCCTCTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTA 1000
15 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTT TGAGAGATGT
16 TTCAGTGTGTT GGACAAAGGT GGGGATTGTA TGCCGCGACT ATCAATAGTC 1100
17 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
18 CGCTGGTACA ATACGGGATT AGAGCGTGTG TGGGGACCGG ATTCTAGAGA 1200
19 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
20 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTGCA 1300
21 ACAGTTTCCC AATTAACAAG AGAAATTAT AGCAACCCAG TATTAGAAAA
22 TTTGATGGT AGTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
23 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCATT TTATACTGAT
24 GTGCATAGAG GCTTTAATTG TTGGTCAGGG CATCAAATAA CAGCTCTCC 1500
25 TGTAGGGTTT TCAGGACCAAG AATTGCGATT CCCTTTATTT GGGAAATGCGG
26 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
27 AGAACATTAT CTTCACCTT ATATAGAAGA ATTATACTTG GTTCAGGGCCC
28 AAATAATCAG GAACTGTTTG TCCTTGATGG AACGGAGTTT TCTTTTGCCCT 1700
29 CCCTAACGAC CAACTTGCC TCCACTATAT ATAGACAAAG GGGTACAGTC
30 GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
31 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
32 GAGCAGTTA CACCTTGAGA GCTCAACGT (stop HD-1)
33 (start HD-73) CCT ATGTTCTCTT
34 GGATACATCG TAGTGTGAA TTTAATAATA TAATTGCACTC GGATAGTATT 1800
35 ACTCAAATCC CTGCACTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
36 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
37 GAAATAACAT TCAGAAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
38 TCGACATCTA CCAGATATCG AGTTCGTGTG CGGTATGCTT CTGTAACCCC 2000
39 GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTC TCCAATACAG
40 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100
41 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
42 TGTTAGAAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTGAAAT 2200
43 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
44 CAGAAGGCGG TGAATGCGCT GTTACGCTC ACAAAACCAAC TAGGGCTAAA 2300
45 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
46 ATTTATCGGA TGAATTGTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
47 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTAC TCCAAGATTC
48 AAATTTCAA GACATTAATA GGCAACCCAGA ACGTGGGTGG GGCAGGAAGTA 2500
49 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
50 ACACTATCAG GTACCTTGA TGAGTGTAT CCAACATATT TGTATCAAAA 2600
51 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT

52 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTG 2700
 53 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTCCTTAT GGCGCTTC
 54 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGGCCAC 2800
 55 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGAA TGGAGAAAAG
 56 TGTGCCCATC ATTGCGATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 57 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 58 AAGATGGGCA CGCAAGACTA GGGAACTCTAG AGTTTCTCGA AGAGAAACCA 3000
 59 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAATGGAG
 60 AGACAAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 61 CAAAAGAATC TGAGATGCT TTATTTGTAAC ACTCTCAATA TGATCAATTA
 62 CAAGCGGATA CGAAATATTGC CATGATTCA GCGGCAGATA AACGTGTTCA 3200
 63 TAGCATTGCA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CGGGGTGTCA
 64 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 65 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 66 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 67 AACGTTCGGT CCTTGTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 68 GTTCGTGTCT GTCCGGGTG TGCTATATC CTTCTGTGTC CAGCGTACAA 3500
 69 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA
 70 CAGACGAACG GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 71 AACACGGTAA CGTGTAAATGA TTATACGTAA AATCAAGAAG AATACGGAGG
 72 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700
 73 CTGATTATGTC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 74 GAGAACCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 75 AGTTGGTTAT GTGACAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
 76 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900
 77 GAATTACTCC TTATGGAGGA A (end HD-73).

1 27. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAAAATC GGTTACACCC CAATCGATAT 500
 9 TTCTTGTGCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTC TGGTCCCTCT 600
 11 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
 12 AGAAGAATTG CACTAGGAACC AAGCCATTTC TAGATTGAA GGACTAAGCA 700
 13 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCCCTTTTG TGCAAGTCAA AATTATCAAG
 16 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTACAA TTTATCAGTT 900
 17 TTGAGAGATG TTTCAGTGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAS ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT

22 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
 23 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
 24 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 25 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
 26 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
 27 TGGAACATATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
 28 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 29 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 31 GAACGGTAGA TTCGCTGAAT GAAATACCAG CACAGAATAA CAACGTGCCA
 32 CCTAGGGCAAG AATTAGTCA TCGATTAAAGC CATGTTTCAA TGTTTCGTT 1700
 33 AGGCTTAAAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 34 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 35 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 36 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 37 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
 38 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCGGGTAAG 2100
 39 AATTGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
 40 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 41 AATTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA
 42 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300
 43 CAGGCAATGA AGTTTATATA GATCBAATTG AATTTGTTCC GGCAGAAGTA
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 45 GCTGTTACT TCTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
 47 TGCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG
 48 ACTTAGTGAT GAGCGGAATT TACTTCAGA TCCAAACTTC AGAGGGATCA 2600
 49 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 50 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAATAGAT GAGTCGAAAT
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 54 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTCGCA 3000
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 58 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 59 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CATTAGTAG GAGAAGCGCT
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 61 TGGAAATGGGA AACAAATATC GTTTATAAG AGGCAAAAGA ATCTGTAGAT
 62 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 63 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
 65 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 66 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 69 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGGAGGGA TATGGAGAAG
 70 GTTGCGTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA

72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCCTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT A TCGTCAGTC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAC T CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 28. A recombinant DNA transfer vector comprising
2 DNA having the following nucleotide sequence or
3 equivalent nucleotide sequences containing bases whose
4 translated region codes for the same amino acid
5 sequence:

| | | (start HD-73) | | ATG | GATAACAATC | 400 |
|----|--------------|---------------|-------------------|---------|------------|-------------|
| 6 | CGAACATCAA | TGAATGCATT | CCTTATAATT | GT | TTAAGTAA | CCCTGAAGTA |
| 7 | GAAGTATTAG | GTGGAGAAAG | AATAGAAACT | GG | TACACCC | CAATCGATAT |
| 8 | TTCCCTGTG | CTAACGCAAT | TTCTTTGAG | TGA | ATTGTT | CCCGGTGCTG |
| 9 | GATTGTGTT | AGGACTAGTT | GATATAATAT | GGGG | AAATTT | TGGTCCCTCT |
| 10 | CAATGGGACG | CATTTCTTGT | ACAAATTGAA | CAG | TTAATT | ACCAAAGAAT |
| 11 | AGAAGAATT | GCTAGGAACC | AAGCCATTTC | TAG | ATTAGAA | GGACTAAGSCA |
| 12 | ATCTTATCA | AATTACGCA | GAATCTTTA | GAG | AGTGGGA | AGCAGATCCT |
| 13 | ACTAATCCAG | CATTAAGAGA | AGAGATGCGT | ATT | CAATTCA | ATGACATGAA |
| 14 | CAGTGCCCTT | ACAAACCGCTA | TTCTCTTTT | TG | CAGTTCAA | AATTATCAAG |
| 15 | TTCCCTTTT | ATCAGTATAT | GTTCAGCTG | CAA | ATTTACA | TTTATCAGTT |
| 16 | TTGAGAGATG | TTTCAGTGT | TGGACAAAGG | TGGGG | ATTG | ATGCCGCGAC |
| 17 | TATCAATAGT | CGTTATAATG | ATTTAACTAG | GCTT | TATTGGC | AACTATACAG |
| 18 | ATTATGCTGT | ACGCTGGTAC | AATAACGGGAT | TAG | AAACGTGT | ATGGGGACCG |
| 19 | GATTCTAGAG | ATTGGGTAAG | GTATAATCAA | TTT | AGAAGAG | AATTAAACACT |
| 20 | AACTGTATTA | GATATCGTTG | CTCTGTTCCC | GAATT | TATGAT | AGTAGAAGAT |
| 21 | ATCCAATT | CGAACAGTTCC | CAATTAAACAA | GAGAA | ATTTTA | TACAAACCCA |
| 22 | GTATTAGAAA | ATTTTGATGG | TAGTTTCTGA | GG | CTCGGCTC | AGGGCATAGA |
| 23 | AGGAAGTATT | AGGAGTCCAC | ATTTGATGGA | TATA | CTTAAC | AGTATAACCA |
| 24 | TCTATACGGA | TGCTCATAAA | <u>GG</u> GAATATT | ATTGG | TCAAGG | GCATCAAATA |
| 25 | ATGGCCTCTC | CTGTAAGGTT | TTCCGGGGCCA | GAATT | CACTT | TTCCGCTATA |
| 26 | TGGAACATATG | GGAAATGCA | CTCCACAAACA | ACG | TATTGTT | GCTCAACTAG |
| 27 | GTCA | GGGGCGT | GTATAGAAACA | TTAT | CGTCCA | CTTTATATAG |
| 28 | AATATAGGGA | TAAATAATCA | ACAAC | TTG | TGACG | GGACAGAATT |
| 29 | TGCTTATGGA | ACCTCCTCAA | ATTG | CTT | GTATAC | AGAAAAAGCG |
| 30 | GAACGGTAGA | TTCGCTGGAT | GAAATACCGC | CG | CTGTATAC | CAACGTGCCA |
| 31 | CCTAGGCAAG | GATTTAGTCA | TCSATTAAAGC | CTG | TTCAA | TGTTTCGTT |
| 32 | AGGCTTTAGT | AATAGTAGTG | TAAGTATAAT | AAG | GCT | (end hd-73) |
| 33 | (start HD-1) | CCAACGT | TTT | CTTGCA | GCATCGCAGT | 1900 |
| 34 | GCTGAATT | ATAATATAAT | TC | CTT | CATCA | CAAATTACAC |
| 35 | AACAAATCT | ACTAATCTTG | GCT | CTGGAAC | TT | CTGTGCGTT |
| 36 | GATTACAGG | AGGAGATATT | CTT | CGAAGAA | CTT | CACCTGG |
| 37 | ACCTTAAGAG | TAAATATTAC | TG | CACCA | CCAGATT | TCACAAAGAT |
| 38 | AATT | CGCTAC | GCTTCTACTA | CAA | ATT | CCATACA |
| 39 | ATT | CGCTAC | CAA | ATT | TACA | TCAATTGACG |

40 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA
 42 CTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 44 ACCTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
 45 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
 47 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 48 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 49 ATAGACAACG AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 50 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATASTCAA 2800
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA
 54 TGTCGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAAGCCCAA AGTCCAATCG 2900
 55 GAAAGSTGTGG AGAGCCGAAT CGATGCGCSC CACACCTTGA ATGGAATCCT
 56 GACTTAGATT GTTCGTGTAG GGATGGAGGAA AAGTGTGCC 3000
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 58 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 59 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAACGCGCT
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAGGAAAT 3200
 61 TGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 62 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAAATAT 3300
 63 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAACGTT
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGSC TATTTTGAA 3400
 65 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 66 TGTCATTAAGA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTG GGTCTTGTGTT
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTACCAA GAAGTTCGTG TCTGTCCGGG 3600
 69 TCGTGGCTAT ATCCTCGTG TCACAGCGTA CAAGGAGGGG TATGGAGAAG
 70 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700
 71 AGCAACTGCG TAGAAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAAGCT CCTTCCGTC CAGCTGATT TGCGTCAGTC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCC AAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACACGC GTGGAAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 29. The DNA transfer vector of claim 25 trans-
 2 ferred to and replicated in a prokaryotic or lower
 3 eukaryotic microorganism.

1 30. The DNA transfer vector of claim 26 transferred to and replicated in a prokaryotic or lower
2 eukaryotic microorganism.

1 31. The DNA transfer vector of claim 27 transferred to and replicated in a prokaryotic or lower
2 eukaryotic microorganism.

1 32. The DNA transfer vector of claim 28 transferred to and replicated in a prokaryotic or lower
2 eukaryotic microorganism.

1 33. Plasmid pEW1 as shown in FIGURE 1 of the
2 drawings.

1 34. Plasmid pEW2 as shown in FIGURE 2 of the
2 drawings.

1 35. Plasmid pEW3 as shown in FIGURE 3 of the
2 drawings.

1 36. Plasmid pEW4 as shown in FIGURE 4 of the
2 drawings.

1 37. Plasmid PACB-1, having the construction of
2 plasmid pEW3 except that the DNA encoding aspartic
3 acid at position 411 is converted to encode asparagine,
4 and the DNA encoding glycine at position 425 is con-
5 verted to encode glutamic acid.

1 38. Plasmid pSYW1, having the construction of plasmid
2 pEW3 except that the DNA encoding arginine at position
3 289 is converted to encode glycine, the DNA encoding
4 arginine at position 311 is converted to encode lysine,
5 and the DNA encoding tyrosine at position 313 is conver-
6 ted to encode glutamate.

1 39. A microorganism transformed by the transfer
2 vector of claim 25.

1 40. A microorganism transformed by the transfer
2 vector of claim 26.

1 41. A microorganism transformed by the transfer
2 vector of claim 27.

1 42. A microorganism transformed by the transfer
2 vector of claim 28.

1 43. E. coli (pEW3), a microorganism according
2 to claim 39.

1 44. E. coli (pEW4), a microorganism according to
2 claim 40.

1 45. E. coli (pACB-1), a microorganism according
2 to claim 41.

1 46. E. coli (pSYW1), a microorganism according
2 to claim 42.

1 47. A process for preparing pesticidal chimeric
2 toxin EW3 having the following amino acid sequence:

3 M D N N P N I N E C I F Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V
8 Q N Y Q V P F L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G

14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
 17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
 18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 21 I D G R P I N Q G N F S A T M M S S G S N L Q S G S F R T V G
 22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 29 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D
 30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
 32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pEW3, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
 50 C G A A C A T C A A T G A A T G C A T T C C T T A T A A T T G T T A A G G T A A G G T A 500
 51 G A A G T A T T A G G T G G A G A A A G A A T A G A A A C T G G T T A C A C C C C A A T C G A T A T 600
 52 T T C C T T G T C G C T A A C G C A A T T T C T T T G A G G T G A A T T T G T T C C C G G T G C T G
 53 G A T T T G T G T T A G G A C T A G T T G A T A T A T A T G G G G A A T T T T T G G T C C C T C 700
 54 C A A T G G G A C G C A T T T C T T G T A C A A A T T G A A C A G T T A A T T A C C C A A A G A A T
 55 A G A A G A A T T C G C T A G T G G A A C C A G C C A T T T C T A G A T T A G A A G G A C T A A G C A 800
 56 A T C T T T A T C A A A T T T A C G C A G A T C T T T A G A G A G T G G G G A A G C A G A T C C T
 57 A C T A A T C C A G C A T T A A G A G A G A G A G A T G C G T A T T C A A T T C A A T G A C A T G A A 900
 58 C A G T G C C C T T A C A A A C C G C T A T T C C T C T T T G C A G T T C A A A T T T A C A A T T A T C A A G
 59 T T C C T C T T T A T C A G T A T A T G T T C A A G C T G C A A A T T T A C A A T T A T C A G T T 900
 60 T T G A G A G A T G T T C A G T G T T T G G A C A A A G G T G G G G A T T T G A T G C C G C G A C

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATAACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATGGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
66 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
69 ATGGCTTCTC CTGAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
70 TGGAACTATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG GATTAGTCA TCGATTAAGC CATGTTCAA TGTTCGTTC 1700
76 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
78 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
80 GATTACAGG AGGAGATATT CTTGAAAGAA CTTCACCTGG CCAGATTTC
81 ACCTTAAGAG TAAATATTAC TGACCACTTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
87 ACCTTTGAGG CAGAATATGA TTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTACT TCTTCAAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500
90 TGTCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
92 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAATAGAT GAGTCGAAAT
95 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATASTCAA 2800
96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
97 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900
98 GAAAGTGTGG AGAGCGGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC CTCATTGCA 3000
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
102 CTAGGSAATC TAGAGTTCTC CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GASAGACAAA CGTAAAAAT 3200
104 TGGAAATGGGA AACAAATATC GTTATATAAG AGGCAAAAGA ATCTGTAGAT
105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
106 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAACGCTT
107 ATCTGCTGAA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
108 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
109 TGTCATTTAA AATGGTGATT TTAATTAATGG CTTATCCTGC TGGAACGTGA 3500
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT
111 CTTCCGAAAT GGGAAAGCAGA AGTGTCAACAA GAAGTTCGTG TCTGTCCGGG 3600
112 TCGTGGCTAT ATCCCTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG
113 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
114 AGCAACTGCG TAGAAGAGGAA AATCTATCCA AATAACACGG TAACGTGTAA

M12C1FDF3D2

115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
117 TATGAAGAAA AATCGTATAAC AGATGGACGA AGAGAGAACATC CTTGTGAATT 3900
118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
120 GAAACCGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
121 GGAA (end HD-1).

1 48. A process for preparing pesticidal chimeric
2 toxin EW4 having the following amino acid sequence:

3 MDNNPNI N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
8 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
13 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
14 P E F A F F L F G N A G N A A P P V L V S L T G L G I F R T
15 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
16 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
17 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
18 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
19 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
20 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
21 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
22 F G Y F E S A N A F T T S S L G N I V G V R N F S G T A G V I
23 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
24 T S T N D L G L K T N V T D Y H I D Q V S N L V T Y L S D E
25 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
26 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
27 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
28 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
29 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
30 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
31 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
32 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
33 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
34 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
35 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
36 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
37 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
38 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
39 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
40 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
41 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
42 S V E L L L M E E

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pEW4, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same amino
48 acid sequence:

49 (start HD-1) ATGG ATAACAATCC GAACATCAAT
 50 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
 51 TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTGCG
 52 TAACGCAATT TCTTTGAGT GAATTGTTTC CCGGTGCTGG ATTGTTGTTA 700
 53 GGACTAGTTG ATATAATATG GGGAAATTTT GBTCCCTCTC AATGGGACGC
 54 ATTTCCTGTA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800
 55 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
 56 ATTTACGCAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
 57 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCTTA
 58 CAACCGCTAT TCCTCTTTG GCAGTTCAA ATTATCAAGT TCCTCTTTA 1000
 59 TCAGTATATG TTCAAGCTGC AAATTACAT TTATCAGTT TGAGAGATGT
 60 TTCAGTGTGTT GGACAAAGGT GGGGATTGTA TGCCGCGACT ATCAATAGTC 1100
 61 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
 62 CGCTGGTACA ATACGGGATT AGAGCGTGTG TGGGGACCAG ATTCTAGAGA 1200
 63 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
 64 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTGCA 1300
 65 ACAGTTTCCC AATTAACAAG AGAAATTAT ACAGAACCCAG TATTAGAAAA
 66 TTTTGATGGT AGTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
 67 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
 68 GTGCATAGAG GCTTTAATTG TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
 69 TGTAGGGTTT TCAGGACCCAG AATTGCGATT CCCTTATTG GGGAAATGCGG
 70 GGAATGCAGC TCCACCCGTA CTTGCTCAT TAACGGTTT GGGGATTGTTT 1600
 71 AGAACATTAT CTTCACCTT ATATAGAAGA ATTATACTTG GTTCAGGCC
 72 AAATAATCAG GAACTGTTG TCCTTGATGG AACGGAGTT TCTTTGCGT 1700
 73 CCCTAACGAC CAACTTGCT TCCACTATAT ATAGACAAAG GGGTACAGTC
 74 GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
 75 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
 76 GAGCAGTTA CACCTTGAGA GCTCAACGT (stop HD-1)
 77 (start HD-73) . CCT ATGTTCTCTT
 78 GGATACATCG TAGTGTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
 79 ACTCAAATCC CTGCACTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
 80 TTCAGGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTAA AATAGTAGTG 1900
 81 GAAATAACAT TCAGAAATAGA GGGTATAATTG AAGTTCCAAT TCACTTCCCA
 82 TCGACATCTA CCAGATATCG AGTTGCTGTA CGGTATGCTT CTGTAACCCC 2000
 83 GATTCACTC AACGTTAATT GGGGTAATTG ATCCATTGTTT TCCAATACAG
 84 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100
 85 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
 86 TGTTAGAAAT TTTAGTGGGA CTGCAAGGAGT GATAATAGAC AGATTTGAAT 2200
 87 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

88 CAGAAGGCAGG TGAATGCGCT GTTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300
 89 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 90 ATTTATCGGA TGAATTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 91 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTAC TCCAAGATTC
 92 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500
 93 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 94 ACACTATCAG GTACCTTGT TGAGTGTCTAT CCAACATATT TGTATCAAAA 2600
 95 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT
 96 ATATCGAAGA TAGTCAAGAC TTAGAAAATCT ATTTAATTGCG CTACAATGCA 2700
 97 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCGCCTTTC
 98 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 99 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGAA TGGAGAAAAG
 100 TGTGCCCATC ATTTCGATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 101 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 102 AAGATGGGCA CGCAAGACTA GGGAAATCTAG AGTTTCTCGA AGAGAAAACCA 3000
 103 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 104 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGGG 3100
 105 CAAAAGAACATC TGAGATGCT TTATTGTAAG ACTCTCAATA TGATCAATT
 106 CAAGCGGATA CGAATATTGCG CATGATTGAT GCGGCAGATA AACGTGTTCA 3200
 107 TAGCATTCGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 108 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 109 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 110 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 111 AACGTTCGGT CCTTGTGTT CCGGAATGGG AAGCAGAAAGT GTCACAAGAA
 112 GTTCTGTCT GTCCGGGTCTG TGGCTATATC CTTCTGTCTA CAGCGTACAA 3500
 113 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA
 114 CAGACGAACT GAAGTGTAGC AACTCGTAG AAGAGGAAAT CTATCCAAT 3600
 115 AACACGGTAA CGTGTAAATGA TTATACGTAA AATCAAGAAG AATACGGAGG
 116 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700
 117 CTGATTATGCG GTCACTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAAGA
 118 GAGAACCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCAACTACC 3800
 119 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG
 120 TATGGATTGA GATTGGAGAA ACGGAAAGGAA CATTATCGT GGACAGCGTG 3900
 121 GAATTACTCC TTATGGAGGA A (end HD-73).

1 49. A process for preparing pesticidal chimeric
 2 toxin ACB-1 having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 5 V D I I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
 14 P E F T F F P L Y G T M G N A A F Q Q R I V A Q L G Q G V Y R

15 TLSSTLYRPFNIGINNQQLSVLDGTEFA
 16 GTSSNLPSAVYRKSGTVDSLNEIPPQNNNV
 17 PPRQEFSHRLSHVSMFRSGFSNSVSIIRA
 18 PTFSWQHRSAEFNNIIPSSQITQIPLTKST
 19 NLGSGTSVVKGPFGTGGDILRRTSPGQIST
 20 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
 21 IDGRPINQGNFSATMSSGSNLQSGSFRTVG
 22 FTTPFNFNSNGSSVFTLSAHVFNSGN
 23 NEVYID
 24 RIEFVPAEVTFEAEYDLEERAQKAVNELFTS
 25 SNQIGLKTDVTDYHIDQVSNLVECLSDEF
 26 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
 27 GINRQLDRGWRGSTDITIQQGDDVFKENYV
 28 TLLGTFDECYPTLYQKIDESKLKAYTRYQ
 29 LRGYIEDSQDLEIYLI
 30 RYNAKHE
 31 TVNVPGT
 32 GSLWPLSAQSP
 33 IKGKCGEPNRCAP
 34 HLEWNPD
 35 LD
 36 C
 37 S
 38 C
 39 R
 40 D
 41 R
 42 V
 E
 L
 L
 M
 E
 E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 PACB-1, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
 50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GTTACACCC CAATCGATAT 500
 52 TTCCCTGTG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG
 53 GATTGTTAGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 54 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
 55 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
 56 ATCTTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
 57 ACTAATCCAG CATTAAAGAGA AGAGATGCCT ATTCAATTCA ATGACATGAA 800
 58 CAGTGCCCTT ACAACCGCTA TTCCCTTTT TGCAGTTCAA AATTATCAAG
 59 TTCCCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 60 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200
66 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400
70 TGGAACATATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG AATTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTT 1700
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
78 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGAAAC TTCTGTCGTT AAAGGACCG 2000
80 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
81 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTCGCTAC GCTTCTACTA CAAATTACA ATTCACATACA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCAT GTCCTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAAGAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATT 2500
90 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGTG GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
92 ATAGACAACT AGACCGTGGC TGGAGAGGAA STACGGATAT TACCATCCAA
93 GGAGGCAGTG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
94 TGATGAGTGC TATCCAAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
95 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
96 GACTTAAAGAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACASTAAA
97 TGTGCCAGGT ACGGGTTCT TATGGCCGCT TTCAAGCCCAA AGTCCAATCG 2900
98 GAAAGTGTGG AGAGCGGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC CTCATTCGCA 3000
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
102 CTAGGGAAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAS GAGAAGCGCT
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAGAAAT 3200
104 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAAATAT 3300
106 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAAGCTT
107 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400
108 GAATTAGAAG GGCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAAA
109 TGTCAATTAAA AATGGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTT
111 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCTG TCTGTCCGGG 3600
112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG

113 GTTGCCTAAC CATTGAGATCGAGAACATACAGACGA ACTGAAGTTT 3700
114 AGCAACTGCG TAGAAGAGGAA AATCTATCCA AATAACACGG TAACGCTGTA
115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC
117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
118 TAACAGAGGG TATAAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
120 GAAACGGAAG GAAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
121 GGAA (end HD-1).

1 50. A process for preparing pesticidal chimeric
2 toxin SYW1 having the following amino acid sequence:

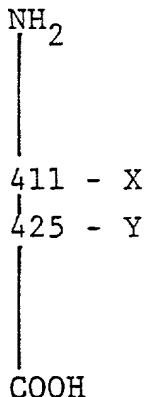
3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y F I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
13 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 S I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V F G T
29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A F S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pSYW1, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCCC CAATCGATAT 500
52 TTCCCTGTCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG
53 GATTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTC TGGTCCCTCT 600
54 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTAA ACCAAAGAAT
55 AGAAGAATTG GCTAGGAACC AAGCCATTC TAGATTAGAA GGACTAAGCA 700
56 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
57 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
58 CAGTGCCCTT ACAACCGCTA TTCCCTTTT TGCAGTTCAA AATTATCAAG
59 TTCCCTCTTT ATCAGTATAT GTTCAAGCTG CAAATTACAA TTTATCAGTT 900
60 TTGAGAGATG TTTCAAGTGTG TGGACAAAGG TGGGGATTTG ATGCCGCGAC
61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAAGAT
65 ATCCAATTGCG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAAACCCA 1200
66 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA
67 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAAA GGGGAATATT ATGGGTCAAGG SCATCAAATA
69 ATGGCTTCTC CTGTAAGGGTT TTGGGGGCCA GAATTCACTT TTCCGCTATA 1400
70 TGGAACATATG GGAATGCAAG CTCCACAAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAAACGGTAGA TTGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG GATTAGTCA TCGATTAAAGC CATGTTCAA TGTTCGTT 1700
76 AGGCTTTAGT AATAGTGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTGGCA SCATCGCAGT 1900
78 GCTGAATTAA ATAATATAAT TCCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
80 GATTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA
81 ACCTTAAGAG TAAATATTAC TGCAACATTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTGCTAC GCTTCTACTA CAAATTACAA ATTCCATACAA TCAATTGACG
83 GAAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500
90 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
92 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA

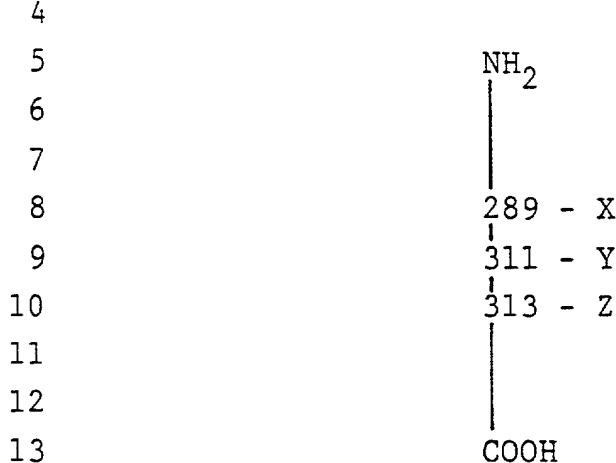
| | | | | | | |
|-----|------------|-------------|-------------|-------------|-------------|------|
| 93 | GGAGGCGATG | ACGTATTCAA | AGAGAATTAC | GTTACGCTAT | TGGGTACCTT | 2700 |
| 94 | TGATGAGTGC | TATCCAACGT | ATTATATATCA | AAAAATAGAT | GAGTCGAAAT | |
| 95 | TAAAAGCCTA | TACCCGTTAT | CAATTAAGAG | GGTATATCGA | AGATAGTCAA | 2800 |
| 96 | GACTTAGAAA | TCTATTAAAT | TCGCTACAAT | GCAAAACATG | AAACAGTAAA | |
| 97 | TGTGCCAGGT | ACGGGTTCT | TATGGCCGCT | TTCAAGCCAA | AGTCCAATCG | 2900 |
| 98 | GAAAGTGTGG | AGAGCCGAAT | CGATGCGCGC | CACACCTTGA | ATGGAATCCT | |
| 99 | GACTTAGATT | GTTCGTTGAG | GGATGGAGAA | AAAGTGTGCC | ATCATTCGCA | 3000 |
| 100 | TCATTTCTCC | TTAGACATTG | ATGTAGGATG | TACAGACTTA | AATGAGGACC | |
| 101 | TAGGTGTATG | GGTGTCTTT | AAGATTAAGA | CGCAAGATGG | GCACGCAAGA | 3100 |
| 102 | CTAGGGAATC | TAGAGTTTCT | CGAAGAGAAA | CCATTAGTAG | GAGAAGCGCT | |
| 103 | AGCTCGTGTG | AAAAGAGCGG | AGAAAAAAATG | GAGAGACAAA | CGTAAAAAAAT | 3200 |
| 104 | TGGAATGGGA | AACAAATATC | GTTTATAAAG | AGGCAAAAGA | ATCTGTAGAT | |
| 105 | GCTTTATTG | TAAACTCTCA | ATATGATCAA | TTACAAAGCGG | ATACGAATAT | 3300 |
| 105 | TGCCATGATT | CATGCGGCCAG | ATAAACGTGT | TCAATAGCATT | CGAGAAGCTT | |
| 107 | ATCTGCCTGA | GCTGTCTGTG | ATTCGGGTG | TCAATGCGGC | TATTTTTGAA | 3400 |
| 108 | GAATTAGAAG | GGCGTATTTT | CACTGCATTC | TCCCTATATG | ATGCGAGAAA | |
| 109 | TGTCATTAAA | AATGGTGATT | TTAATAATGG | CTTATCCTGC | TGGAACGTGA | 3500 |
| 110 | AAGGGCATGT | AGATGTAGAA | GAACAAAACA | ACCAACCTTC | GGTCCTTGT | |
| 111 | CTTCCGGAAT | GGGAAGCAGA | AGTGTACCAA | GAAGTTCGTG | TCTGTCCGGG | 3600 |
| 112 | TCGTGGCTAT | ATCCTTCGTG | TCACAGCGTA | CAAGGGAGGG | TATGGAGAAAG | |
| 113 | GTTGCGTAAC | CATTGATGAG | ATCGAGAAACA | ATACAGACGA | ACTGAAGTTT | 3700 |
| 114 | AGCAACTGCG | TAGAAGAGGA | AATCTATCCA | AATAACACGG | TAACGTGTAA | |
| 115 | TGATTATACT | GTAAATCAAG | AAGAATACGG | AGGTGCCTAC | ACTTCTCGTA | 3800 |
| 116 | ATCGAGGATA | TAACGAAGCT | CCTTCCGTAC | CAGCTGATT | TGCGTCACTC | |
| 117 | TATGAAGAAA | AAATCGTATAC | AGATGGACGA | AGAGAGAAATC | CTTGTGAATT | 3900 |
| 118 | TAACAGAGGG | TATAGGGATT | ACACGCCACT | ACCAGTTGGT | TATGTGACAA | |
| 119 | AAGAATTAGA | ATACTTCCCA | GAAACCGATA | AGGTATGGAT | TGAGATTGGA | 4000 |
| 120 | GAAACGGAAG | GAACATTAT | CGTGGACAGC | GTGGAATTAC | TCCTTATGGA | |
| 121 | GGAA | (end HD-1). | | | | |

1 51. A chimeric toxin, having the amino acid
2 sequence of toxin EW3, with changes which can be shown
3 schematically as follows:



13 wherein X is one of the 20 common amino acids
14 except Asp when the amino acid at position 425 is
15 Gly; Y is one of the 20 common amino acids except
16 Gly when the amino acid at position 411 is Asp.

1 52. A chimeric toxin, having the amino acid
2 sequence of toxin EW3, with changes which can be shown
3 schematically as follows:



15 wherein X is one of the 20 common amino acids except
16 Arg when the amino acid at position 311 is Arg and the
17 amino acid at position 313 is Tyr; Y is one of the 20
18 common amino acids except Arg when the amino acid at
19 position 289 is Arg and the amino acid at position 313
20 is Tyr; and Z is one of the 20 common amino acids
21 except Tyr when the amino acid at position 289 is
22 Arg and the amino acid at position 311 is Arg.

1 53. DNA encoding a chimeric toxin as shown in
2 claim 51.

1 54. DNA encoding a chimeric toxin as shown in
2 claim 52.

1 55. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 51.

1 56. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 52.

1 57. A chimeric toxin comprising the variable
2 region or regions of two or more Bacillus toxins.

1 58. A toxin, according to claim 57, wherein the
2 Bacillus toxins are B. thuringiensis toxins.

1 59. A toxin, according to claim 58, wherein the
2 B. thuringiensis toxins are B. thuringiensis var.
3 kurstaki HD-1 toxin and B. thuringiensis var. kurstaki
4 HD-73 toxin.

1 60. A toxin, according to claim 58, wherein
2 the B. thuringiensis toxins are encoded by a pesticide-
3 producing strain of Bacillus thuringiensis, consisting
4 of B. thuringiensis M-7, B. thuringiensis var. kurstaki,
5 B. thuringiensis var. finitimus, B. thuringiensis var.
6 alesti, B. thuringiensis var. sotto, B. thuringiensis
7 var. dendrolimus, B. thuringiensis var. kenyae, B.
8 thuringiensis var. galleriae, B. thuringiensis var.
9 canadensis, B. thuringiensis var. entomocidus, B.
10 thuringiensis var. subtoxicus, B. thuringiensis var.
11 aizawai, B. thuringiensis var. morrisoni, B. thuringiensis
12 var. ostriniae, B. thuringiensis var. tolworthi, B.
13 thuringiensis var. darmstadiensis, B. thuringiensis
14 var. toumanoffi, B. thuringiensis var. kyushuensis, B.
15 thuringiensis var. thompsoni, B. thuringiensis var.
16 pakistani, B. thuringiensis var. israelensis, B. thurin-
17 giensis var. indiana, B. thuringiensis var. dakota,

18 B. thuringiensis var. tohokuensis, B. thuringiensis
19 var. kumanotoensis, B. thuringiensis var. tochigiensis,
20 B. thuringiensis var. colmeri, B. thuringiensis var.
21 wuhanensis, B. thuringiensis var. tenebrionis, B.
22 thuringiensis var. thuringiensis, and other Bacillus
23 species selected from B. cereus, B. moritai, B.
24 popilliae, B. lentimorbus, and B. sphaericus.